

## Original article

## Identification of multiple HLA-A\*0201-restricted cruzipain and FL-160 CD8<sup>+</sup> epitopes recognized by T cells from chronically *Trypanosoma cruzi*-infected patients

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Received 20 August 2004; accepted 17 January 2005

Available online 21 March 2005

### Abstract

Chronic Chagas disease occurs in 16 million individuals chronically infected by the protozoan *Trypanosoma cruzi* in Latin America, and may lead to a dilated cardiomyopathy in 10–30% of patients. A vigorous cellular immune response holds parasitism in check. However, up to now, few *T. cruzi* proteins have been shown to be recognized by CD8<sup>+</sup> T cells from Chagas disease patients. In this study, we designed 94 peptides derived from *T. cruzi* proteins cruzipain and FL-160, predicted to bind to HLA-A2 molecules. After in vitro binding assays to HLA-A\*0201, 26 peptides were selected, and their recognition by PBMC from Chagas disease patients was tested with the IFN- $\gamma$  ELISPOT assay. All 26 peptides were recognized by PBMC from at least one patient. Furthermore, a tetrameric HLA-A\*0201 complex built with the cruzipain 60–68 peptide that was frequently recognized in the periphery also bound to CD8<sup>+</sup> T cells from a heart-infiltrating T cell line obtained from a single patient with Chagas disease cardiomyopathy. Thus, our results suggest that the recognition of CD8<sup>+</sup> T cell epitopes in cruzipain and FL-160 may have a pathogenic or protective role in chronic Chagas disease.

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**Keywords:** CD8<sup>+</sup> T cells; Chagas disease; ELISPOT; Tetramer; Epitopes

### 1. Introduction

Chagas disease is caused by the intracellular protozoan parasite *Trypanosoma cruzi* and affects 16–18 million people in Latin America. Most patients survive the acute phase of the disease, remaining asymptomatic for many years. However, 10–30% of patients develop an inflammatory dilated CD8<sup>+</sup> T cell-rich cardiomyopathy (Chagas disease cardiomy-

opathy, CCC), with a fatal outcome in 30% of cases [1,2]. The heart inflammatory mononuclear infiltrate is known to play a pathogenic role in CCC. Because of the lack of a vaccine and effective treatment during the chronic phase, CCC is still a major public health problem in many countries.

Experiments in murine models of *T. cruzi* infection have suggested that CD8<sup>+</sup> T cells are involved in the control of infection. It has been demonstrated that mice deficient for  $\beta$ 2-microglobulin, MHC class I or CD8<sup>+</sup> T cells showed a higher parasitemia than normal littermates during the acute phase of infection [3–6]. Furthermore, CD8<sup>+</sup> T cells are the

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predominant lymphocyte population present in the heart tissue of mice chronically infected with *T. cruzi*, and the depletion of the CD8<sup>+</sup> T cell population increases the number of parasite nests in the heart during acute infection [7]. Recently, it was shown that cytotoxic T lymphocytes (CTL) from PBMC of Chagas disease patients displayed cytotoxicity and IFN- $\gamma$  production against epitopes of amastigote-stage surface protein-1 (ASP-1), ASP-2 and trypomastigote-form surface antigen-1 (TSA-1) from the trans-sialidase family of *T. cruzi* proteins [8,9]. However, there are limited data on *T. cruzi*-specific memory CD8<sup>+</sup> T cells from Chagas disease patients and no direct data showing whether heart-infiltrating CD8<sup>+</sup> T cells from CCC patients recognize *T. cruzi* epitopes.

In order to investigate the recognition of *T. cruzi* epitopes by CD8<sup>+</sup> T cells from Chagas disease patients, we have screened 94 nonamer and decamer peptides from cruzipain (CZ) [10] and FL-160 (FL) [11] predicted to bind to HLA-A2 with an in vitro HLA-A2 binding assay, given the high frequency of this HLA allele in the Brazilian population [12]. Cruzipain and FL-160 are secreted/membrane proteins from *T. cruzi* [11,13–15], with a high likelihood of being presented by the MHC class I pathway [16]. The IFN- $\gamma$  ELISPOT assay was performed in PBMC from Chagas disease patients with peptides selected from those submitted to binding assays. In order to detect parasite-specific CD8<sup>+</sup> T cells in heart lesions of CCC patients, we used HLA-A\*0201-cruzipain and FL-160 peptide tetrameric complexes.

## 2. Material and methods

### 2.1. Patient and control samples

Peripheral blood of 12 Chagas disease patients (10 CCC and two asymptomatic; 11 HLA-A2 positive and one HLA-A2 negative) was collected with anticoagulant (heparin for cell cultures or EDTA) for this study. Six HLA-A2-positive *T. cruzi* seronegative, healthy individuals, were used as controls. Heart-infiltrating T cells were obtained from a trans-venous endomyocardial biopsy sample from the patient #11, diagnosed as severe CCC, with positive serology for *T. cruzi*. Sample collection procedures have been approved by the Internal Review Board, School of Medicine, University of São Paulo.

Chagas disease patients and healthy individuals were typed for HLA-A2 using a SSP-PCR reaction. DNA was obtained from peripheral blood samples collected with EDTA by DTAB/CTAB method as described [17]. The sequence-specific primers used in PCR reaction to HLA-A2 were 5': TGG ATA GAG CAG GAG GGT 3' and 5': CAA GAG CGC AGG TCC TCT 3'.

### 2.2. PBMC and PBMC-derived T cell lines

Mononuclear cells from heparinized peripheral blood samples were obtained by Ficoll gradient centrifugation.

Peptide-induced PBMC-derived T cell lines ( $5 \times 10^6$  per well) from Chagas disease patients were established with  $5 \mu\text{g/ml}$  of peptide stimulus every week in the presence of  $10^6$  irradiated PBMC per ml as feeder cells (50 Gy) in 1 ml of Dulbecco's Modified Eagle's medium supplemented with 2 mM of L-glutamine, 1 mM sodium pyruvate, MEM's non-essential amino acids and MEM's vitamins (all from GIBCO, Grand Island, NY, USA), 50  $\mu\text{g/ml}$  of gentamicin, 10 mM HEPES buffer, 10% of normal human serum (complete medium) plus IL-2 (100 U/ml, Proleukin IL-2, Chiron, USA), IL-7 (5 ng/ml, PeproTech, NJ, USA) and IL-15 (5 ng/ml, PeproTech) in a humidified, 5% of CO<sub>2</sub> atmosphere, in order to test the specificity of tetramer complexes.

### 2.3. Heart-infiltrating T cell line

Endomyocardial biopsy fragments from HLA-A2<sup>+</sup> patient #11 were minced and cultured in 96-well flat-bottom culture plates in DMEM (Gibco) with 10% of inactivated human serum, supplemented with 40 U/ml IL-2 (Hoffman-La Roche, Nutley, NJ, USA), in the presence of autologous irradiated (50 Gy) PBMC ( $10^5$  per well) as described [18]. Lymphoblasts were later expanded by two 15-day rounds of restimulation with PHA (5  $\mu\text{g/ml}$ ), 50 Gy-irradiated PBMC ( $10^6$  per ml) in complete medium plus 40 U/ml of IL-2. After two rounds of expansion, lymphoblasts were cultured in DMEM 10% of human serum supplemented by IL-2 (100 U/ml), IL-7 (5 ng/ml) and IL-15 (5 ng/ml) and stimulated by PHA. CD8<sup>+</sup> cells were purified using magnetic beads attached to a monoclonal antibody against human CD8 (M450, Dynal). The beads were removed using Detach-a-Bead antibodies (Dynal, Oslo). No *T. cruzi* parasite growth was observed during endomyocardial biopsy explant cultures as detected by direct visualization of the highly mobile trypomastigote forms.

### 2.4. Selection of synthetic peptides and binding assay

The sequences of *T. cruzi* proteins—cruzipain (A45629, gi:323055) [13] and FL-160 (JH0823, gi:542406) [11]—were scanned using a computer algorithm to identify 9- and 10-mer sequences binding to HLA-A\*0201 [19,20]. Ninety-four peptides were selected and synthesized using solid-phase Fmoc with amidated C-terminals (Chiron) and analyzed by reverse-phase high performance liquid chromatography (Shimadzu, Tokyo, Japan). Peptide quality was assessed by Maldi-Tof mass spectrometry (Micromass, UK). The binding affinity of the synthetic peptides to purified soluble HLA-A2.1 molecules was quantified by measuring the binding inhibition of a radiolabeled standard probe peptide as described [21]. Peptides with a high affinity for HLA-A\*0201 ( $\text{IC}_{50} < 500 \text{ nM}$ ), as well as some peptides showing undetectable binding to HLA-A\*0201, were selected for ELISPOT assay. These sequences were re-synthesized using solid phase technology using (Fmoc) strategy as described [22,23], and peptide quality analyzed as described above.

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